

**Applicant:** Rosana Kapeller-Libermann  
**Title:** 47174, A NOVEL HUMAN GLYCOSYLTRANSFERASE  
AND USES THEREFOR  
**Attorney/Agent:** Jean M. Silveri  
**Docket No.:** MPI00-418P1RDV1M  
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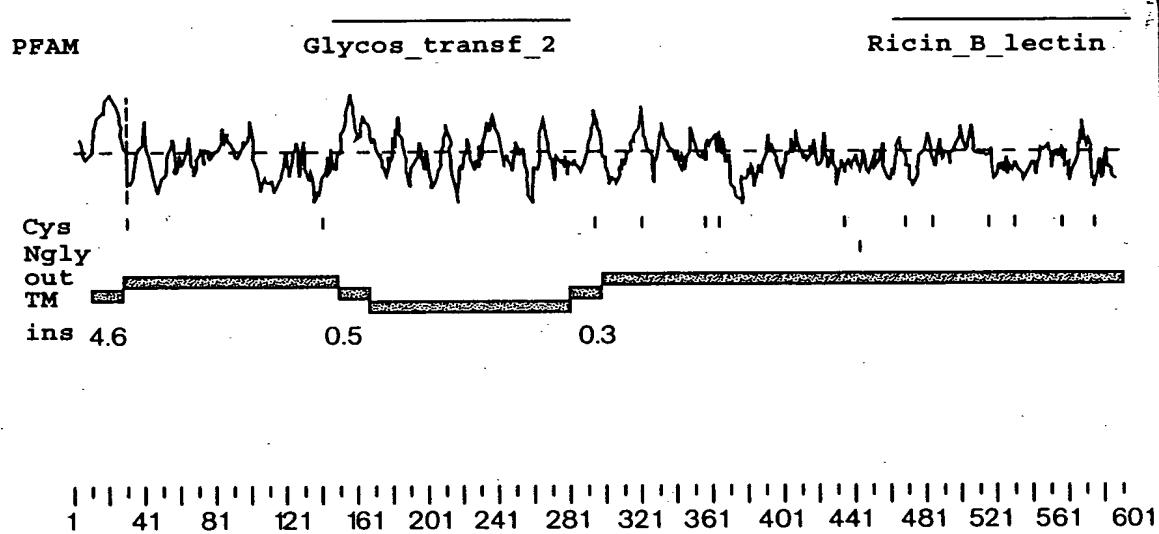


Fig. 1

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Glycos\_transf\_2: domain 1 of 1, from 154 to 336: score 55.7, E = 1e-12  
\*->sivIptYNeeadyLeelleSvlaqs.tledieiivvDDgSetDetve  
s+v + Ne+++ +++ ++Sv + + + e+i vDD+S + e++  
47174 154 SVVFIFVNEALSVILRSVHSVNHTpSQLLKEVILVDDNSDNVELKF 200  
iaedylderikeenpriiivirleensqGpaaArnkgirratGdsdyIlf  
++ y+ ++ +p + ++r+++ G +Ar +g ++at ++ f  
47174 201 NLDQYV---NKRYPGLVKIVRNSRRE-GLIRARLQGWKAATAP--VVGF 243  
LDaDdiftpdkleklyeaatdaavvlgaida.....yeayaegesnlyr  
+Da+++f ++ e++++++ +++ +vl+aid + +++e +++ + ++  
47174 244 FDAHVEFNTGWAEPALSRIEDRRRIVLPAIDNikystFEVQQYANA-AH 292  
iaradterslfagllrktrgtgglesfeigsnaiyrreafeelf<-\*  
++++ ++ ++ ++ +r g+ ++ +++++ + ++ ++++e+f  
47174 293 GYNWGLWCMYIIPPPQDWLDR--GDESAPIRTPAMIGCSFVVDREYF 336

Fig. 2

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Alignments of top-scoring domains:

ricin\_3: domain 1 of 1, from 465 to 595: score 32.5, E = 9.8e-06

\*>rgyfliiggntglCLdvngnseksdGnpvg1wdChgggnQ1WkltY  
+g ++ + ++ CLd +++++ + +l++Chq ++Q1 +++  
47174 465 YGEVRNSK-ASAYCLDQGAEDGD-----RAILYPCHGMSSQLVRY5- 504  
nesdgairi.....nsdlCLtvng...tvttlysCdgtdkgndnQk.  
dg + ++ +++ + +CL +g+++ tl++C++ + + Q+  
47174 505 --ADGLLQLgplgstaflPDSKCLVDDGtgrMPTLKKCEDV--ARPTQRL 550  
WevnkdgcircrnPknskkgvds glcLdvkdgn.....kvqlwtcnsgdap  
W + ++g i+++ +g cL+v +++ + + + + + C+g  
47174 551 WDFTQSGPIVSR-----ATGRCLEVEMSKdanfglRLVVQRC5G---- 589  
nQkWife<-\*  
QkW ++  
47174 590 -QKWMIR 595

Fig. 3

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>2308 p99.2 (23) PAGT(3) // N-ACETYLGALACTOSAMINYLTRANSFERASE TRANSFERASE  
POLYPEPTIDE ACETYLGALACTOSAMINYLTRANFERASE UDP-GALNAC:POLYPEPTIDE  
GLYCOSYLTRANSFERASE PROTEIN-UDP PROTEIN-UDP N-  
LENGTH = 172

Score = 423 (154.0 bits), Expect = 4.7e-40, P = 4.7e-40  
Identities = 77/151 (50%), Positives = 104/151 (68%)

Query: 312 RGDESAPIRTPAMIGCSFVVDRGYFDIGLLDPGMEVYGGENVELGMRVWQCGGSMEVLP 371  
R D + PIR+P M G F +++EYF ++G DPGM+++GGEN+EL RVWQCGG +E++P  
Sbjct: 14 RKDPTDPIRSPTMAGGLFAINKKEYFEELGTYDPGMDIWGGENLELSFRVWQCGGRLEIVP 73

Query: 372 CSRVAAHIERTRKPYNNNDIYYAK---RNALRAAEVWMDDFKSHVYMAWNIPMSNPGVDF 427  
CS V H+ R R PY K RN +R AEVWMDD+K + Y + P + DF  
Sbjct: 74 CSHVGHVFRKRSPYTFFPGKGSGKDVISRNTVRVAEVWMDDYKEYFYK--HNPQARKVRDF 131

Query: 428 GDVSERLALRQRLKCRSFKWYLENVPEMRV 458  
GD+SER LR++L+C+SFKWYLENVYP++ V  
Sbjct: 132 GDISERKELREKLQCKSFKWYLENVYPDLYV 162

Fig. 4